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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/759,508B

DATE: 10/01/2001

TIME: 13:55:46

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Output Set: N:\CRF3\10012001\I759508B.raw

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3 <110> APPLICANT: Fishman, Mark C.
5 <120> TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
7 <130> FILE REFERENCE: 00786/381002
9 <140> CURRENT APPLICATION NUMBER: US 09/759,508B
10 <141> CURRENT FILING DATE: 2001-01-12
12 <150> PRIOR APPLICATION NUMBER: US 60/175,787
13 <151> PRIOR FILING DATE: 2000-01-12
15 <160> NUMBER OF SEQ ID NOS: 11
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 81940
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
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26 <222> LOCATION: (133)..(80910)
27 <223> OTHER INFORMATION:
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35 gtgcctagaa ag atg aca act caa gca ccg acg ttt acg cag ccg tta caa      171
36      Met Thr Thr Gln Ala Pro Thr Phe Thr Gln Pro Leu Gln
37      1          5          10
39 agc gtt gtg gta ctg gag ggt agt acc gca acc ttt gag gct cac att      219
40 Ser Val Val Val Leu Glu Gly Ser Thr Ala Thr Phe Glu Ala His Ile
41      15          20          25
43 agt ggt ttt cca gtt cct gag gtg agc tgg ttt agg gat ggc cag gtg      267
44 Ser Gly Phe Pro Val Pro Glu Val Ser Trp Phe Arg Asp Gly Gln Val
45 30          35          40          45
47 att tcc act tcc act ctg ccc ggc gtg cag atc tcc ttt agc gat ggc      315
48 Ile Ser Thr Ser Thr Leu Pro Gly Val Gln Ile Ser Phe Ser Asp Gly
49      50          55          60
51 cgc gct aaa ctg acg atc ccc gcc gtg act aaa gcc aac agt gga cga      363
52 Arg Ala Lys Leu Thr Ile Pro Ala Val Thr Lys Ala Asn Ser Gly Arg
53      65          70          75
55 tat tcc ctg aaa gcc acc aat gga tct gga caa gcg act agt act gct      411
56 Tyr Ser Leu Lys Ala Thr Asn Gly Ser Gly Gln Ala Thr Ser Thr Ala
57      80          85          90
59 gag ctt ctc gtg aaa gct gag aca gca cca ccc aac ttc gtt caa cga      459
60 Glu Leu Leu Val Lys Ala Glu Thr Ala Pro Pro Asn Phe Val Gln Arg
61      95          100          105
63 ctg cag agc atg acc gtg aga caa gga agc caa gtg aga ctc caa gtg      507
64 Leu Gln Ser Met Thr Val Arg Gln Gly Ser Gln Val Arg Leu Gln Val
65 110          115          120          125
67 aga gtg act gga atc cct aca cct gtg gtg aag ttc tac cgg gat gga      555
68 Arg Val Thr Gly Ile Pro Thr Pro Val Val Lys Phe Tyr Arg Asp Gly
69      130          135          140

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71	gcc gaa atc cag agc tcc ctt gat ttc caa att tca caa gaa ggc gac	603
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73	145 150 155	
75	ctc tac agc tta ctg att gca gaa gca tac cct gag gac tca ggg acc	651
76	Leu Tyr Ser Leu Leu Ile Ala Glu Ala Tyr Pro Glu Asp Ser Gly Thr	
77	160 165 170	
79	tat tca gta aat gcc acc aat agc gtt gga aga gct act tcg act gct	699
80	Tyr Ser Val Asn Ala Thr Asn Ser Val Gly Arg Ala Thr Ser Thr Ala	
81	175 180 185	
83	gaa tta ctg gtt caa ggt gaa gaa gaa gta cct gct aaa aag aca aag	747
84	Glu Leu Leu Val Gln Gly Glu Glu Glu Val Pro Ala Lys Lys Thr Lys	
85	190 195 200 205	
87	aca att gtt tcg act gct cag atc tca gaa tca aga caa acc cga att	795
88	Thr Ile Val Ser Thr Ala Gln Ile Ser Glu Ser Arg Gln Thr Arg Ile	
89	210 215 220	
91	gaa aag aag att gaa gcc cac ttt gat gcc aga tca att gca aca gtt	843
92	Glu Lys Lys Ile Glu Ala His Phe Asp Ala Arg Ser Ile Ala Thr Val	
93	225 230 235	
95	gag atg gtc ata gat ggt gcc gct ggg caa cag ctg cca cat aaa aca	891
96	Glu Met Val Ile Asp Gly Ala Ala Gly Gln Gln Leu Pro His Lys Thr	
97	240 245 250	
99	cct ccc agg att cct ccg aag cca aag tca aga tcc cca aca cca ccg	939
100	Pro Pro Arg Ile Pro Pro Lys Ser Arg Ser Pro Thr Pro Pro	
101	255 260 265	
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104	Ser Ile Ala Ala Lys Ala Gln Leu Ala Arg Gln Gln Ser Pro Ser Pro	
105	270 275 280 285	
107	ata aga cac tcc cct tcc ccg gtc aga cac gtg cgg gca ccg acc cca	1035
108	Ile Arg His Ser Pro Ser Pro Val Arg His Val Arg Ala Pro Thr Pro	
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116	Ile Arg Ser Val Arg Ser Pro Leu Leu Met Arg Lys Thr Gln Ala Ser	
117	320 325 330	
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120	Thr Val Ala Thr Gly Pro Glu Val Pro Pro Pro Trp Lys Gln Glu Gly	
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123	tac gtg gcc tcc tca tct gag gct gag atg aga gag aca acg ctg aca	1227
124	Tyr Val Ala Ser Ser Ser Glu Ala Glu Met Arg Glu Thr Thr Leu Thr	
125	350 355 360 365	
127	acc tct act cag atc agg aca gaa gag aga tgg gaa ggg aga tac ggt	1275
128	Thr Ser Thr Gln Ile Arg Thr Glu Glu Arg Trp Glu Gly Arg Tyr Gly	
129	370 375 380	
131	gtc cag gag caa gtg acc atc agt ggt gct gcg ggt gct gcc gcc agt	1323
132	Val Gln Glu Gln Val Thr Ile Ser Gly Ala Ala Gly Ala Ala Ala Ser	
133	385 390 395	
135	gtg tcg gcc agt gct agc tac gca gca gag gct gtt gcc act ggt gct	1371

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140	Lys	Glu	Val	Lys	Gln	Asp	Ala	Asp	Lys	Ser	Ala	Ala	Val	Ala	Thr	Val	
141		415					420				425						
143	ggt	gct	gcc	ggt	gat	atg	gcc	aga	gtg	aga	gaa	cca	gtg	atc	agc	gct	1467
144	Val	Ala	Ala	Val	Asp	Met	Ala	Arg	Val	Arg	Glu	Pro	Val	Ile	Ser	Ala	
145	430					435					440					445	
147	gta	gag	cag	act	gct	cag	agg	aca	acc	acg	act	gct	gtg	cac	atc	caa	1515
148	Val	Glu	Gln	Thr	Ala	Gln	Arg	Thr	Thr	Thr	Thr	Ala	Val	His	Ile	Gln	
149				450						455					460		
151	cct	gct	caa	gaa	cag	gta	aga	aag	gaa	gcg	gag	aag	act	gct	gta	act	1563
152	Pro	Ala	Gln	Glu	Gln	Val	Arg	Lys	Glu	Ala	Glu	Lys	Thr	Ala	Val	Thr	
153			465				470				475						
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156	Lys	Val	Val	Ala	Ala	Asp	Lys	Ala	Lys	Glu	Gln	Glu	Leu	Lys	Ser		
157		480					485				490						
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160	Arg	Thr	Lys	Glu	Ile	Ile	Thr	Thr	Lys	Gln	Glu	Gln	Met	His	Val	Thr	
161		495					500				505						
163	cat	gag	cag	ata	aga	aaa	gaa	act	gaa	aaa	aca	ttt	gta	cca	aag	gta	1707
164	His	Glu	Gln	Ile	Arg	Lys	Glu	Thr	Glu	Lys	Thr	Phe	Val	Pro	Lys	Val	
165	510					515					520				525		
167	gta	att	tcc	gca	gct	aaa	gcc	aaa	gaa	caa	gaa	act	aga	att	tct	gaa	1755
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172	Glu	Ile	Thr	Lys	Lys	Gln	Lys	Gln	Val	Thr	Gln	Glu	Ala	Ile	Met	Lys	
173			545				550				555						
175	gaa	act	agg	aaa	aca	ggt	gta	cct	aaa	gtc	ata	ggt	gcc	aca	ccc	aaa	1851
176	Glu	Thr	Arg	Lys	Thr	Val	Val	Pro	Lys	Val	Ile	Val	Ala	Thr	Pro	Lys	
177		560					565				570						
179	gtc	aaa	gaa	caa	gat	tta	gta	tca	aga	ggt	aga	gaa	ggc	att	act	acc	1899
180	Val	Lys	Glu	Gln	Asp	Leu	Val	Ser	Arg	Gly	Arg	Glu	Gly	Ile	Thr	Thr	
181		575				580					585						
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184	Lys	Arg	Glu	Gln	Val	Gln	Ile	Thr	Gln	Glu	Lys	Met	Arg	Lys	Glu	Ala	
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188	Glu	Lys	Thr	Ala	Leu	Ser	Thr	Ile	Ala	Val	Ala	Thr	Ala	Lys	Ala	Lys	
189			610				615				620						
191	gaa	caa	gaa	aca	ata	ctg	aga	act	aga	gaa	act	atg	gct	act	aga	caa	2043
192	Glu	Gln	Glu	Thr	Ile	Leu	Arg	Thr	Arg	Glu	Thr	Met	Ala	Thr	Arg	Gln	
193			625				630				635						
195	gaa	caa	atc	caa	ggt	acc	cat	gga	aag	gtg	gac	ggt	gga	aaa	aag	gct	2091
196	Glu	Gln	Ile	Gln	Val	Thr	His	Gly	Lys	Val	Asp	Val	Gly	Lys	Lys	Ala	
197		640					645				650						
199	gaa	gct	gta	gca	aca	ggt	ggt	gct	gca	gta	gac	cag	gcc	cga	gtc	aga	2139
200	Glu	Ala	Val	Ala	Thr	Val	Val	Ala	Ala	Val	Asp	Gln	Ala	Arg	Val	Arg	

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207	act ttg gag tac gga tat aag gaa cgc att tcc gcc gca aag gta gct	2235		
208	Thr Leu Glu Tyr Gly Tyr Lys Glu Arg Ile Ser Ala Ala Lys Val Ala			
209	690 695 700			
211	gag cct ccc caa cgt cca gcc tca gaa ccc cac gtt gtc cct aaa gca	2283		
212	Glu Pro Pro Gln Arg Pro Ala Ser Glu Pro His Val Val Pro Lys Ala			
213	705 710 715			
215	gtc aag cct aga gta atc cag gct cct tct gag act cat atc aaa act	2331		
216	Val Lys Pro Arg Val Ile Gln Ala Pro Ser Glu Thr His Ile Lys Thr			
217	720 725 730			
219	act gat caa aag gga atg cac ata tca tca cag atc aag aaa act aca	2379		
220	Thr Asp Gln Lys Gly Met His Ile Ser Ser Gln Ile Lys Lys Thr Thr			
221	735 740 745			
223	gat cta aca acg gaa aga tta gtc cat gtg gat aaa cgc ccc cgc aca	2427		
224	Asp Leu Thr Thr Glu Arg Leu Val His Val Asp Lys Arg Pro Arg Thr			
225	750 755 760 765			
227	gct agc cct cac ttt act gtt tca aaa att tct gtt cct aag aca gaa	2475		
228	Ala Ser Pro His Phe Thr Val Ser Lys Ile Ser Val Pro Lys Thr Glu			
229	770 775 780			
231	cat gga tat gag gca tca ata gcc ggt agt gct att gcc aca tta caa	2523		
232	His Gly Tyr Glu Ala Ser Ile Ala Gly Ser Ala Ile Ala Thr Leu Gln			
233	785 790 795			
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237	800 805 810			
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243	aca ccc ttg cca cag ttc ccc ttc gct gac aca cca gat act tac aag	2667		
244	Thr Pro Leu Pro Gln Phe Pro Phe Ala Asp Thr Pro Asp Thr Tyr Lys			
245	830 835 840 845			
247	agt gaa gct ggc gtt gag gtg aaa aag gaa gta ggg gtg agc atc act	2715		
248	Ser Glu Ala Gly Val Glu Val Lys Lys Glu Val Gly Val Ser Ile Thr			
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251	ggc acc acc gtc cgt gaa gag cgc ttt gaa gta ctg cac gga cgc gaa	2763		
252	Gly Thr Thr Val Arg Glu Glu Arg Phe Glu Val Leu His Gly Arg Glu			
253	865 870 875			
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257	880 885 890			
259	gtt act cca cca act ttg gtc tcg ggc tta aaa aat gtg act gtc ata	2859		
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263	gaa ggt gaa tct gtc acc ttg gag tgc cac atc tct gga tac cca tcc	2907		
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271	gac	ttc	cag	ata	acc	ttc	cag	agt	gga	att	gct	cgt	ctt	atg	att	cgc	3003
272	Asp	Phe	Gln	Ile	Thr	Phe	Gln	Ser	Gly	Ile	Ala	Arg	Leu	Met	Ile	Arg	
273				945					950					955			
275	gaa	gca	ttt	gcg	gaa	gac	agc	ggg	cga	ttt	act	tgc	agt	gct	gta	aat	3051
276	Glu	Ala	Phe	Ala	Glu	Asp	Ser	Gly	Arg	Phe	Thr	Cys	Ser	Ala	Val	Asn	
277			960					965					970				
279	gag	gct	gga	acc	gtc	agc	aca	tcc	tgc	tat	ctg	gct	gtg	cag	gtg	tca	3099
280	Glu	Ala	Gly	Thr	Val	Ser	Thr	Ser	Cys	Tyr	Leu	Ala	Val	Gln	Val	Ser	
281		975					980					985					
283	gaa	gaa	ttt	gaa	aag	gaa	acc	aca	gcc	gtg	act	gag	aaa	ttt	act	aca	3147
284	Glu	Glu	Phe	Glu	Lys	Glu	Thr	Thr	Ala	Val	Thr	Glu	Lys	Phe	Thr	Thr	
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293				1025						1030					1035		
295	cct	tac	ttt	att	aca	aaa	cca	gtg	gtc	cag	aaa	ctg	gtg	gaa	ggg		3282
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312	Val	Ile	Ser	Met	Thr	Phe	Ala	Asp	Asp	Ala	Gly	Glu	Tyr	Thr	Ile		
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